

SEQUENCE LISTING

<110> Pfizer Inc

<120> Novel Polypeptide

<130> PC10914ADAM

<140>

<141>

<150> 0008504.3

<151> 2000-04-05

<150> 60/198,367

<151> 2000-04-19

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 993

<212> DNA

<213> Homo sapiens

<400> 1

atggaaccaa atggcacctt cagcaataac aacagcagga actgcacaat tgaaaacttc 60
aagagagaat ttttcccaat tgtatatctg ataatatatt tctggggagt cttgggaaat 120
gggttgtcca tatatgtttt cctgcagcct tataagaagt ccacatctgt gaacgttttc 180
atgctaaatc tggccatttc agatctcctg ttcataagca cgcttcctt cagggctgac 240
tattatctta gaggctccaa ttggatatatt ggagacctgg cctgcaggat tatgtcttat 300
tccttgatg tcaacatgta cagcagtatt tatttctga ccgtgctgag tgttgtgcgt 360
ttcctggcaa tgggtcaccc ctttcggctt ctgcatgtca ccagcatcag gaggcctgg 420
atcctctgtg ggatcatatg gatccttata atggcttccct caataatgct cctggacagt 480
ggctctgagc agaacggcag tgtcacatca tgcttagagc tgaatctcta taaaattgct 540
aagctgcaga ccatgaacta tattgccttg gtgggtgggt gcctgctgcc atttttcaca 600
ctcagcatct gttatctgct gatcattcgg gttctgttaa aagtggaggt cccagaatcg 660

gggctgcggg tttctcacag gaaggcactg accaccatca tcatcacctt gatcatcttc 720
 ttcttgtggt tcctgcccta tcacacactg aggaccgtcc acttgacgac atggaaagtg 780
 ggtttatgca aagacagact gcataaagct ttggttatca cactggcctt ggcagcagcc 840
 aatgcctgct tcaatcctct gctctattac tttgctgggg agaattttta ggacagacta 900
 aagtctgcac tcagaaaagg ccattccacag aaggcaaaga caaagtgtgt tttccctggt 960
 agtgtgtggt tgagaaagga aacaagagta taa 993

<210> 2

<211> 330

<212> PRT

<213> Homo sapiens

<400> 2

Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr
 1 5 10 15

Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
 20 25 30

Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
 35 40 45

Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
 50 55 60

Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
 65 70 75 80

Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
 85 90 95

Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
 100 105 110

Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
 115 120 125

Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
 130 135 140

Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser

145		150		155		160
Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu						
	165		170		175	
Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val						
	180		185		190	
Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile						
	195		200		205	
Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val						
	210		215		220	
Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe						
225		230		235		240
Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr						
	245		250		255	
Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val						
	260		265		270	
Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu						
	275		280		285	
Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu						
	290		295		300	
Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val						
305		310		315		320
Ser Val Trp Leu Arg Lys Glu Thr Arg Val						
	325		330			

<210> 3
 <211> -24
 <212> DNA
 <213> Homo sapiens

<400> 3
 accatggaga gaaaatttat gtcc

24

<210> 4
 <211> 22
 <212> DNA

<213> Homo sapiens

<400> 4

ttatactctt gtttcctttc tc

22

<210> 5

<211> 1041

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1041)

<400> 5

atg gag aga aaa ttt atg tcc ttg caa cca tcc atc tcc gta tca gaa 48

Met Glu Arg Lys Phe Met Ser Leu Gln Pro Ser Ile Ser Val Ser Glu

1

5

10

15

atg gaa cca aat ggc acc ttc agc aat aac aac agc agg aac tgc aca 96

Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr

20

25

30

att gaa aac ttc aag aga gaa ttt ttc cca att gta tat ctg ata ata 144

Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile

35

40

45

ttt ttc tgg gga gtc ttg gga aat ggg ttg tcc ata tat gtt ttc ctg 192

Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu

50

55

60

cag cct tat aag aag tcc aca tct gtg aac gtt ttc atg cta aat ctg 240

Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu

65

70

75

80

gcc att tca gat ctc ctg ttc ata agc acg ctt ccc ttc agg gct gac 288

Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp

85

90

95

tat tat ctt aga ggc tcc aat tgg ata ttt gga gac ctg gcc tgc agg 336

Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg

100

105

110

att atg tct tat tcc ttg tat gtc aac atg tac agc agt att tat ttc 384

Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe

115

120

125

ctg acc gtg ctg agt gtt gtg cgt ttc ctg gca atg gtt cac ccc ttt	432
Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe	
130 135 140	
cgg ctt ctg cat gtc acc agc atc agg agt gcc tgg atc ctc tgt ggg	480
Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly	
145 150 155 160	
atc ata tgg atc ctt atc atg gct tcc tca ata atg ctc ctg gac agt	528
Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser	
165 170 175	
ggc tct gag cag aac ggc agt gtc aca tca tgc tta gag ctg aat ctc	576
Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu	
180 185 190	
tat aaa att gct aag ctg cag acc atg aac tat att gcc ttg gtg gtg	624
Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val	
195 200 205	
ggc tgc ctg ctg cca ttt ttc aca ctc agc atc tgt tat ctg ctg atc	672
Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile	
210 215 220	
att cgg gtt ctg tta aaa gtg gag gtc cca gaa tgc ggg ctg cgg gtt	720
Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val	
225 230 235 240	
tct cac agg aag gca ctg acc acc atc atc atc acc ttg atc atc ttc	768
Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe	
245 250 255	
ttc ttg tgt ttc ctg ccc tat cac aca ctg agg acc gtc cac ttg acg	816
Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr	
260 265 270	
aca tgg aaa gtg ggt tta tgc aaa gac aga ctg cat aaa gct ttg gtt	864
Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val	
275 280 285	
atc aca ctg gcc ttg gca gca gcc aat gcc tgc ttc aat cct ctg ctc	912
Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu	
290 295 300	
tat tac ttt gct ggg gag aat ttt aag gac aga cta aag tct gca ctc	960
Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu	
305 310 315 320	

Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
 180 185 190

Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
 195 200 205

Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
 210 215 220

Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
 225 230 235 240

Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
 245 250 255

Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
 260 265 270

Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
 275 280 285

Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
 290 295 300

Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
 305 310 315 320

Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
 325 330 335

Ser Val Trp Leu Arg Lys Glu Thr Arg Val
 340 345